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GGACATGGAGGGAAAGTTCTACAGAGGAGGCACAGTGGGCTTCAGGAACACCCTGCTTGAGAGGCCTG
TGAGAGGTGGGGAATCAATACCTGACCTCGCTCTCCTTCCATCTCTCCCCAACCCACAGGGGTTGGTG
TGGGCCCCACAGGCGAGCCTCCCGGGGAGAGAAGTGGAGAGAGGACCTGGAGGGCCAGTAGAAGGTAT
GCACACAAGTATCTACAAGGCACCAGGCATTTTTTGAGCATTTGGGATTTGTCAGCAAACAAGTCAGA
CAAAAAACCTTGCTCTGGTGGAGGGAACATTCTAGCAAAGGAAGGCAAATGACAAGCAGGAGAAGTAT
TTGCTAAGA**ATG**GCAATCCTGACGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAATATCCCA
TGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCAACATGA
CTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGACATTTGCTCTCGACAT
CGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCTATGGTGTAATTTGAGAATCATTCAC**TG**
AGCATCAACTATGTAACCAGCATTGGGTTGGGTGCCAGAGATCCAAAGCTAAGACACCAAAACCTGCT
CTCCAGGAAACGAGAGGCTGAGAAGAGGGCCAGCAGGTGTCTGTCAGTACTTGGAGCCGTGAGAGCAG
GGAGTGGGTGCTGGGCTGAGGAACCAGAGGTAATGGCCCTGGGGACGCCCGGGAAGAGATGAGTTTTG
AGGCAAAGGGATTTGCATTTGTGGATGAACTTGTGTGTTCAGCTGAAGGCTGAAGTTGTAACTCTGAA
CCACAGGACAAAGCATGATGTGATGTCTTCCTCACTAAATGGCAATGTCCTTGAGAAGACCCTGTCTT
AATCATCTCTGTGTCTCACGCCTGGCTCATAACATATGCTTATCGCATGCTTTTAATAAAAGGAGGAA
AATGC

FIG._1A

AAAAAATACAGCAGGTGAAGGAGGTTGGAGAGTAGGGGGTGGAGGGCCCACGCAGCACTTGTCCTTCA
CCCTGGAGGGGATCTGTTACATGCCCCAGATTGCTGGTCCCCTAGAAATGTTACTGAGGCAGCCTCTG
CATTTTTGCAGGGATTGTTTTCTACTGTTTGACATTCACGTAACCTCCTAACGCTGTCTGGGGAAGAT
GCTACCCCCTGCTCTCCCCGTCTTTCCTGCACTCTCAGCAATGGGATGGGCTGACTGATGCCCTGTGG
GCTGGAAAGCTGACCACAGTTGCTGCAGACCAGACCCCCTCACATAGTGAGTGCTGGGCTGAGGAATC
CAGGAGAGCCCGAGGGGGGACACTGAAGGTGTATCGTTGGCCCTGCCAGCTGCAAGTGAACTGCTTCT
GATGAATTTTAATAGGGAGAAAGAAGTATTTGCTAAGA**ATG**GCAATCCTGACGCTCAGCCTTCAACTC
ATCTTGTTATTAATACCATCAATATCCCATGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGA
CCAAGATTGGGCAAACGTCTCCAACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATT
ACCGGAATGCCGACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAG
CTATGGTGTAATTTGAGGTCAGTGGCCAGAGGACAGATCCCGTCTACATTA**TGA**GTGAAGCGGAGAGC
TACTGCAGGGTTCTGAGCAGAGTCCTAATTTATATTTTAGAAGAATCATCATGGCTCCTAGATTAGGA
ATAAAACGAAGGGGCCCAGGGATGGAAACGATGAGTCCAGTTGGGTTACTGCAAAGATCCAGGCCAGA
AATCCAGGCACAGTGGCACACACCTGAGTCCCAGATAATTCCACCTACTGGTCCTGCTCTGTGGCCTA
CTGGTCCGAGTCCAGCCCCGACTGATTTCTGGGCCTGTAATGTCTAAAAACGCTCCCTGCTGATGTTT
TGCAAGTGACTGTGTTACTTGAAGGCAGTTCCTAGGATAAACTAGTCGCTTTATCATTACAGAATCAT
TCACTGAGCATCAACTATGTAACCAGCATTGGGTTGGGTGCCAGAGATCCAAAGCTAAGACACCAAAA
CCTGCTCTCCAGGAAACGAGAGGCTGAGAA

FIG._1C

GGTGGAGCCAAATAAGGGAATGAAAGCAGGCCACCGGAGCCTCGGAGAGGCAACCGTTTGGGGTACTC
TTCCACACTGTGGCAGCTTTGTTCTTTTGCTCTTTGCAGTAAGTTTTGCTGTTGCTTACTCTTTGGGT
CTGCACTGCCTTTATGAACTGTAACACTGACCATGGAGGTCTGCAGCTTCACTCCTCAAGCCAGCAAG
ACCAGGAGCCCACTGGGAGGAGGAATGAACAACTCTGGACACGCCACCCTTAAGAGCTGTAACACTCA
CCGCGACGGTCTGCAGCTTCACTCCTGAAGTCAGCGAGACCACAAACCCACCAGAAGGAAGAAAATCC
GGACACATCTGAACATCTGAGGGAACTCCGCACACACCATCTTTAAGAACTGTAACACTCACCACGAG
GGCCCGTGGCTTCATTCTTGAAGTCAGCAAGACCAAGAACCCACCAATTCTGGACACAACAGGACACA
CACATGGGAGGGGGAGGCCAGAGGGAAACCTAGCTGGCTTGGGGTGGGAATTTGAATCCCTGAGCCCA
TCTTCTTCTTTCACCACTTTGTCCGGTGACATTAGGACCAACCAACCAATGCCATTATATTTCTTAGT
TTACAAGAAAATGTTTGAAGTTCTCATCCACAGAATCACTTAGCTTCTTGCTTTTTACAAGTGGTTGA
TTAGGAGTATTCAATACAGATTTTGTGTATCACTATAAACAGTTCACAGCATGGACTACTGGTGTTCT
CTTTACTAACTGAAATGGTGTCATTAGCACCTTTAAATCTAATCCATTTAGAGAGCCAGTTCCGGAAA
CCTCAGAACCAGTTTGGAAAACTTCCGTTCTTCTGAAGCCATTTTTGGAACCACATCTGTGCTAGGTT
CTCCAGGGAAACAGAACCAATATGTTTTATTTACTATGGGGACTGGCTCATATGATTCTGGAGGCCTA
GAAGTCCCTCCCTCTCAAGATGTGCTGTCAGCAAGCTGCAGAACCAGGAAAGCTGGTGGTGTCAGAGT
CTGAAGGCCTGAGAACTGGGTGGGGAGTGGGACAGACTAAGGGGCCTTTAGTCTCTGGGTTGGTGTGG
TCCCCACAGGTGAGCCTTTCGTGGAGAAGGGTGGAGAGGGGATCTGGAAGGGCCAATAGAAGATACTC
AGCACTAAGAGACCTTTGGACTCAGACCAGAACTTACACCATTCATTCATTCAGTCGGTGAAAATGTA
TTGACCACTGTATCAACCAGGATTGTGACACAAAAACAGATGGCACACTCAAAAGAGGATAATTCAAG
AAGGGCTTCTTTAAGGGACTATTTCCCAAGATGGGAATGGAGGGGAACCTGCAGGGCTAGTGTCCTAC
CCTCCAGCAGGCAGCAGCTAATTCCTGAGGGGATAAGGACGTGGTTGCGAGGACATGGAGGGAAAGTT
CTACAGAGGAGGCACAGTGGGCTTCAGGAACACCCTGCTTGAGAGGCCTGTGAGAGGGATTGTTTTCT
ACTGTTTGACATTCACGTAACCTCCTAACGCTGTCTGGGGAAGATGCTACCCCCTGCTCTCCCCGTCT
TTCCTGCACTCTCAGCAATGGGATGGGCTGACTGATGCCCTGTGGGCTGGAAAGCTGACCACAGTTGC
TGCAGACCAGACCCCCTCACATAGTGAGTGCTGGGCTGAGGAATCCAGGAGAGCCCGAGGGGGGACAC
TGAAGGTGTATCGTTGGCCCTGCCAGCTGCAAGTGAACTGCTTCTGATGAATTTTAATAGGGAGAAAG
AAGTATTTGCTAAGA**ATG**GCAATCCTGATGCTCAGCCTTCAACTCATCTTGTTATTAATACCATCAAT
ATCCCATGAGGCTCATAAAACGAGTCTTTCTTCTTGGAAACATGACCAAGATTGGGCAAACGTCTCCA
ACATGACTTTCAGCAACGGAAAACTAAGAGTCAAAGGCATTTATTACCGGAATGCCGACATTTGCTCT
CGACATCGCGTAACCTCAGCAGGCCTAACTCTGCAGGACCTTCAGCTATGGTGTAATTTGAGGTCAGT
GGCCAGAGGACAGATCCCGTCTACATTA**TGA**GTGAAGCGGAGAGCTACTGCAGGGTTCTGAGCAGAGT
CCTAATTTATATTTTAGAAGAATCATCATGGCTCCTAGATTAGGAATAAAACGAAGGGGCCCAGGGAT
GGAAACGATGAGTCCAGTTGGGTTACTGCAAAGATCCAGGCCAGAAATCCAGGCACAGTGGCACACAC
CTGAGTCCCAGATAATTCCACCTACTGGTCCTGCTCTGTGGCCTACTGGTCCGAGTCCAGCCCCGACT
GATTTCTGGGCCTGTAATGTCTAAAAACGCTCCCTGCTGATGTTTTGCAAGTGACTGTGTTACTTGAA
GGCAGTTCCTAGGATAAACTAGTCGCTTTATC

FIG._1B

MAILTLSLQLILLLIPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVKGIYYRNAD
ICSRHRVTSAGLTLQDLQLWCNLRIIH

Domain Information

Signal peptide:
1-19

N-glycosylation site.
38-42
41-45

FIG._2A

MAILMLSLQLILLLIPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVKGIYYRNAD
ICSRHRVTSAGLTLQDLQLWCNLRSVARGQIPST

Domain Information

Signal peptide:
1-19

N-glycosylation site.
38-42
41-45
N-myristoylation site.
89-95

FIG._2B

MAILTLSLQLILLLIPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLRVKGIYYRNAD
ICSRHRVTSAGLTLQDLQLWCNLRSVARGQIPSTL

Domain Information

Signal peptide:
1-19

N-glycosylation sites
38-42
41-45

N-myristoylation sites
89-95

FIG._2C

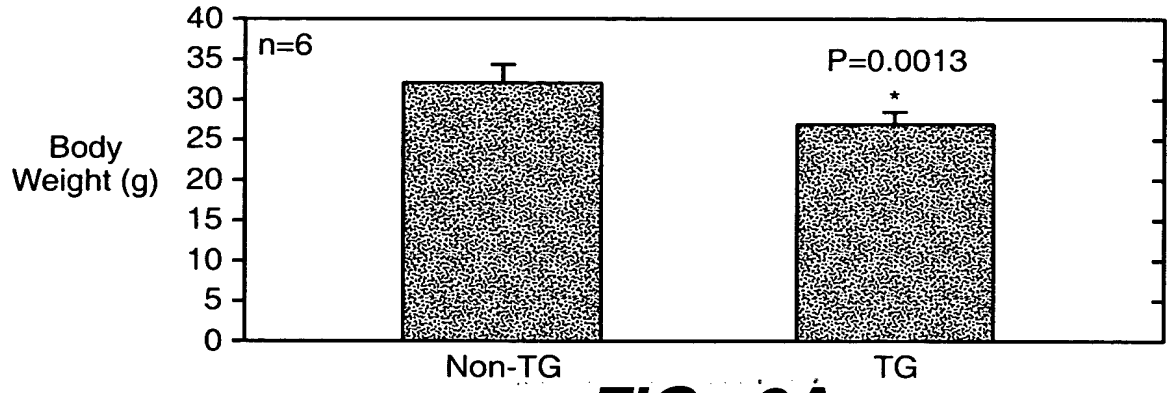

FIG._3A

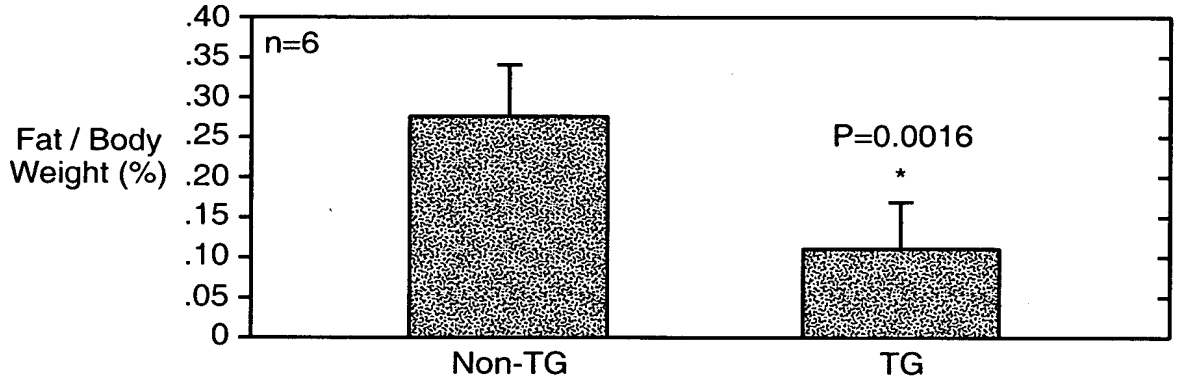

FIG._3B

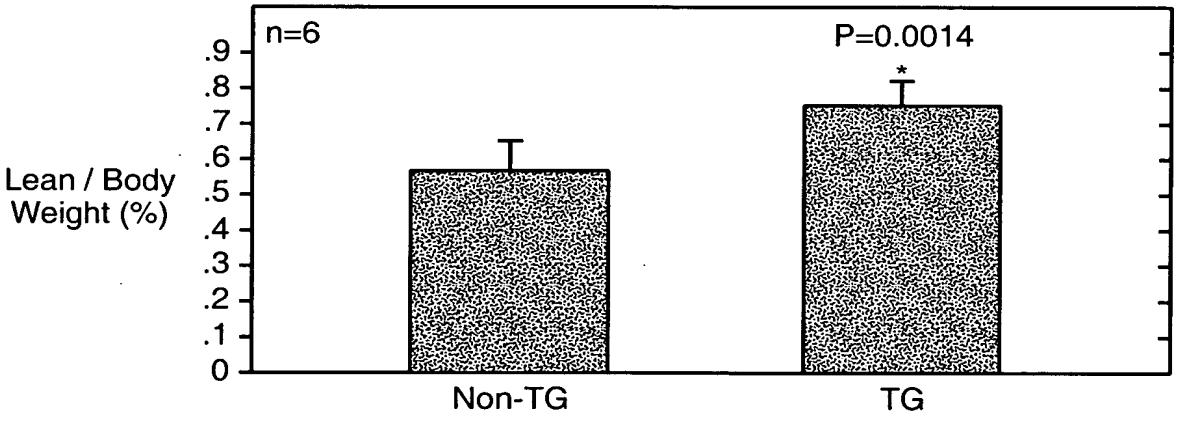

FIG._3C

```
DNA146649      1 MAILTLSLQLILLLIPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLR
DNA149986      1 MAILMLSLQLILLLIPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLR
DNA149995      1 MAILTLSLQLILLLIPSISHEAHKTSLSSWKHDQDWANVSNMTFSNGKLR

DNA146649     51 VKGIYYRNADICSRHRVTSAGLTLQDLQLWCNLRIIH--------
DNA149986     51 VKGIYYRNADICSRHRVTSAGLTLQDLQLWCNLRSVARGQIPSTL
DNA149995     51 VKGIYYRNADICSRHRVTSAGLTLQDLQLWCNLRSVARGQIPSTL
```

FIG._4

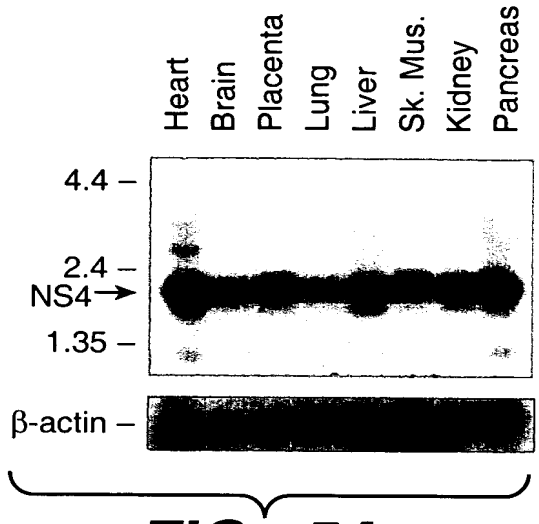

FIG._5A

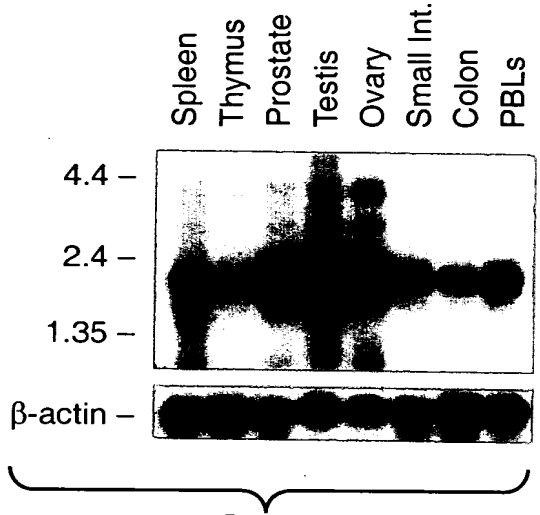

FIG._5B

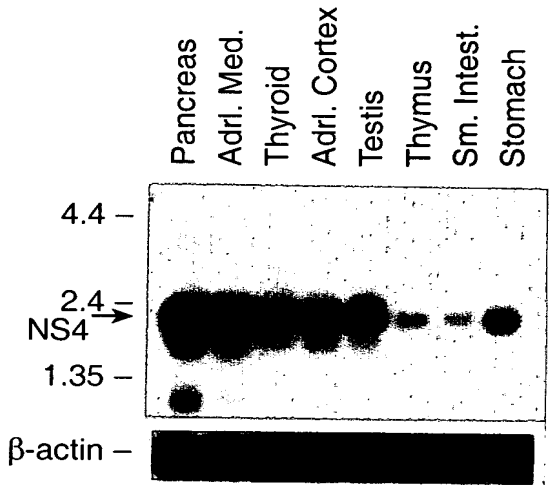

FIG._5C

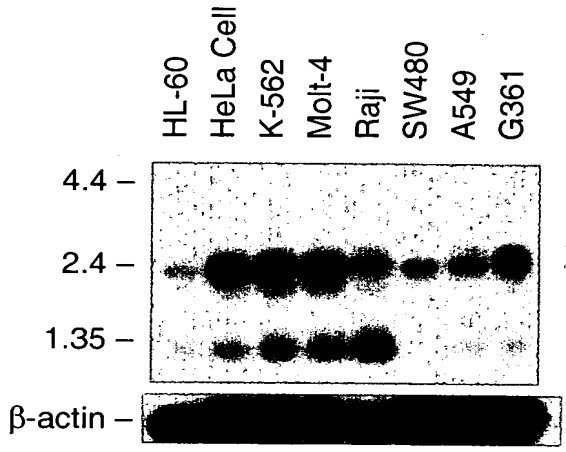

FIG._5D